What is claimed is:

1. A method of analyzing nucleic acids using the polymerase chain reaction (PCR), comprising:

(a) providing a double-stranded population of nucleic acids comprising single-stranded overhangs;

(b) annealing ligate linkers to said population of nucleic acids whereby at least a subset of nucleic acids from said double-stranded population have linkers bound at both ends;

(c) amplifying said subset of nucleic acids by PCR, thereby analyzing said subset of nucleic acids.

2. The method of Claim 1, wherein said population of nucleic acids is a population of genomic DNA fragments.

3. The method of Claim 1, wherein said single-stranded overhangs are derived from restriction enzyme digestions.

4. The method of Claim 1, wherein said ligate linkers comprise a common PCR primer binding site.

5. The method of Claim 1, wherein said ligate linkers comprise a different PCR primer binding site for each different overhang.

6. The method of Claim 3, wherein said restriction enzyme is selected from a group consisting of single Type IIs restriction enzyme, a combination of two or more Type IIs enzymes, and a combination of Type IIs restriction enzyme and other types of restriction enzymes.

7. A method of analyzing a subset of nucleic acids within a nucleic acid population using the polymerase chain reaction (PCR), comprising:

(a) providing a single-stranded population of nucleic acids;

(b) annealing a double-stranded branch primer to at least a subset of said population of nucleic acids;

(c) extending the primer by DNA polymerase;

(d) repeating steps (a) through (c) at least once to produce a subset of nucleic acids that comprise a partially double-stranded primer sequence at both ends;

(e) amplifying said subset of nucleic acids by PCR, thereby analyzing said subset of nucleic acids.

8. The method of Claim 7, wherein said subset of nucleic acids comprises nucleic acid fragments of a first size.

9. A method of analyzing a subset of nucleic acids within a nucleic acid population using the polymerase chain reaction (PCR), comprising:

(a) providing a double-stranded population of nucleic acids that comprise cleaved interrupted palindromic sequences at one or both ends:

(b) annealing an adaptor containing fixed nucleotides onto the said population of nucleic acids thereby producing at least a subset of nucleic acids that comprise an adaptor sequence at both ends:

(c) amplifying said subset of nucleic acids by PCR, thereby analyzing said subset of nucleic acids.

10. The method of Claim 9, wherein said subset of nucleic acids comprises nucleic acid fragments of a first size.

11. The method of Claim 9, wherein said interrupted palindromic sequences comprises palindromic sequences that are interrupted by at least one ambiguous nucleotide.

12. The method of Claim 9, wherein said cleaved interrupted palindromic sequences are derived from restriction enzyme digestions.

13 The method of Claim 12, wherein said restriction enzyme is a single restriction enzyme or a combination of two or more restriction enzymes.

14. The method of Claim 9. wherein said adaptor comprises a single-stranded overhang that has at least one fixed nucleotide.

15. The method of Claim 9. wherein said adaptor comprises a PCR primer binding site.